

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/809,144
Source: IFWD
Date Processed by STIC: 10-18-04

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IFWO

RAW SEQUENCE LISTING

DATE: 10/18/2004

PATENT APPLICATION: US/10/809,144

TIME: 13:56:18

Input Set : A:\03-284-E.ST25.txt

Output Set: N:\CRF4\10182004\J809144.raw

```

3 <110> APPLICANT: The Board of Trustees of the University of Illinois
4      Costa, Robert
5      Raychaudhuri, Pradip
6      Wang, Xinhe
7      Kalinichenko, Vladimir
8      Major, Michael
9      Wang, I-Ching
11 <120> TITLE OF INVENTION: METHODS OF INHIBITING TUMOR CELL PROLIFERATION
13 <130> FILE REFERENCE: 03-284-E
15 <140> CURRENT APPLICATION NUMBER: US 10/809,144
16 <141> CURRENT FILING DATE: 2004-03-25
18 <150> PRIOR APPLICATION NUMBER: US 60/457,257
19 <151> PRIOR FILING DATE: 2003-03-25
21 <150> PRIOR APPLICATION NUMBER: US 60/474,075
22 <151> PRIOR FILING DATE: 2003-10-23
24 <150> PRIOR APPLICATION NUMBER: US 60/540,691
25 <151> PRIOR FILING DATE: 2004-01-30
27 <150> PRIOR APPLICATION NUMBER: US 60/549,691
28 <151> PRIOR FILING DATE: 2004-03-02
30 <160> NUMBER OF SEQ ID NOS: 13
32 <170> SOFTWARE: PatentIn version 3.0
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 2737
36 <212> TYPE: DNA
37 <213> ORGANISM: Homo Sapiens
39 <400> SEQUENCE: 1
40 ggagcccgga gcccgccttc ggagctacgg cctaacggcg gcggcgactg cagtctggag      60
42 ggtccacact tgtgattctc aatggagagt gaaaacgcag attcataatg aaaactagcc      120
44 cccgtcggcc actgattctc aaaagacgga ggctgcccct tcctgttcaa aatgccccaa      180
46 gtgaaacatc agaggaggaa cctaagagat cccctgcccc acaggagtct aatcaagcag      240
48 aggcctccaa ggaagtggca gagtccaact cttgcaagtt tccagctggg atcaagatta      300
50 ttaaccaccc caccatgccc aacacgcaag tagtggccat cccaacaat gctaataatc      360
52 acagcatcat cacagcactg actgccaagg gaaaagagag tggcagtagt gggcccaaca      420
54 aattcatcct catcagctgt gggggagccc caactcagcc tccaggactc cggcctcaaa      480
56 cccaaccag ctatgatgcc aaaaggacag aagtgaccct ggagaccttg ggaccaaac      540
58 ctgcagctag ggatgtgaat cttcctagac cacctggagc cttttgcgag cagaaacggg      600
60 agacctgtgc agatggtgag gcagcaggct gcactatcaa caatagccta tccaacatcc      660
62 agtggcttcg aaagatgagt tctgatggac tgggctcccg cagcatcaag caagagatgg      720
64 aggaaaagga gaattgtcac ctggagcagc gacagggttaa ggttgaggag ccttcgagac      780
66 catcagcgtc ctggcagaac tctgtgtctg agcggccacc ctactcttac atggccatga      840
68 tacaattcgc catcaacagc actgagagga agcgcagtac tttgaaagac atctatacgt      900
70 ggattgagga ccactttccc tactttaagc acattgccaa gccaggctgg aagaactcca      960
72 tccgccacaa cctttccctg cacgacatgt ttgtccggga gacgtctgcc aatggcaagg      1020

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74 tctccttctg gaccattcac cccagtgcc accgctactt gacattggac caggtgttta 1080
76 agcagcagaa acgaccgaat ccagagctcc gccggaacat gaccatcaaa accgaactcc 1140
78 ccctgggccc acggcggaag atgaagccac tgctaccacg ggtcagctca tacctggtac 1200
80 ctatccagtt cccggtgaac cagtcactgg tgttcagcc ctcggtgaag gtgccattgc 1260
82 ccctggcgcc ttccctcatg agctcagagc ttgcccgcc tagcaagcga gtccgcattg 1320
84 cccccaaggt gctgctagct gaggagggga tagctcctct ttcttctgca ggaccaggga 1380
86 aagaggagaa actcctgttt ggagaagggt tttctccttt gcttccagtt cagactatca 1440
88 aggaggaaga aatccagcct ggggaggaaa tgccacactt agcgagaccc atcaaagtgg 1500
90 agagccctcc cttggaagag tggccctccc cggcccccac tttcaaagag gaatcatctc 1560
92 actcctggga ggattcgtcc caatctccca cccaagacc caagaagtcc tacagtgggc 1620
94 ttaggtcccc aaccgggtgt gtctcgaaa tgcttgtgat tcaacacagg gagaggaggg 1680
96 agaggagccg gtctcgagg aaacagcatc tactgcctcc ctgtgtggat gagccggagc 1740
98 tgctcttctc agagggggcc agtacttccc gctggggccc agagctcccg ttcccagcag 1800
100 actcctctga cctgcctccc cagctcagct actcccagga agtgggagga ccttttaaga 1860
102 caccatttaa ggaaacgtg cccatctcct ccaccccgag caaatctgtc ctcccagaa 1920
104 cccctgaatc ctggaggctc acgccccag ccaaagtagg gggactggat ttcagcccag 1980
106 taaaaacctc ccagggtgcc tctgaccctt tgcccgacc cctggggctg atggatctca 2040
108 gcaccactcc cttgcaaagt gtcctcccc ttgaatcacc gcaaaggctc ctcaattcag 2100
110 aacccttaga cctcatctcc gtcccctttg gcaactcttc tccctcagat atagacgtcc 2160
112 ccaagccagg ctcccggag ccacaggttt ctggccttgc agccaatcgt tctctgacag 2220
114 aaggcctggt cctggacaca atgaatgaca gcctcagcaa gatcctgctg gacatcagct 2280
116 ttcttgccct ggacaggac ccactgggcc ctgacaacat caactggctc cagtttattc 2340
118 ctgagctaca gtagagccct gcccttgccc ctgtgtcaa gctgtccacc atcccgggca 2400
120 ctccaaggct cagtgacccc caagcctctg aagtaggaca gcaggcaggg actgttctgc 2460
122 tcctcatagc tccctgctgc ctgattatgc aaaagtagca gtcacaccct agccactgct 2520
124 gggaccttgt gttcccgaag agtatctgat tcctctgctg tccctgccag gagctgaagg 2580
126 gtgggaacaa caaaggcaat ggtgaaaaga gattaggaac ccccagcct gtttccattc 2640
128 tctgcccagc agtctcttac ctccctgat ctttgcaggg tggctcctgt aaatagtata 2700
130 aattctccaa attatcctct aattataaat gtaagct 2737

```

133 <210> SEQ ID NO: 2

134 <211> LENGTH: 748

135 <212> TYPE: PRT

136 <213> ORGANISM: Homo sapiens

138 <400> SEQUENCE: 2

```

140 Met Lys Thr Ser Pro Arg Arg Pro Leu Ile Leu Lys Arg Arg Arg Leu
141 1 5 10 15
143 Pro Leu Pro Val Gln Asn Ala Pro Ser Glu Thr Ser Glu Glu Glu Pro
144 20 25 30
146 Lys Arg Ser Pro Ala Gln Gln Glu Ser Asn Gln Ala Glu Ala Ser Lys
147 35 40 45
149 Glu Val Ala Glu Ser Asn Ser Cys Lys Phe Pro Ala Gly Ile Lys Ile
150 50 55 60
152 Ile Asn His Pro Thr Met Pro Asn Thr Gln Val Val Ala Ile Pro Asn
153 65 70 75 80
155 Asn Ala Asn Ile His Ser Ile Ile Thr Ala Leu Thr Ala Lys Gly Lys
156 85 90 95
158 Glu Ser Gly Ser Ser Gly Pro Asn Lys Phe Ile Leu Ile Ser Cys Gly
159 100 105 110
161 Gly Ala Pro Thr Gln Pro Pro Gly Leu Arg Pro Gln Thr Gln Thr Ser

```

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162		115		120		125											
164	Tyr	Asp	Ala	Lys	Arg	Thr	Glu	Val	Thr	Leu	Glu	Thr	Leu	Gly	Pro	Lys	
165		130					135				140						
167	Pro	Ala	Ala	Arg	Asp	Val	Asn	Leu	Pro	Arg	Pro	Pro	Gly	Ala	Leu	Cys	
168	145					150				155						160	
170	Glu	Gln	Lys	Arg	Glu	Thr	Cys	Ala	Asp	Gly	Glu	Ala	Ala	Gly	Cys	Thr	
171				165					170						175		
173	Ile	Asn	Asn	Ser	Leu	Ser	Asn	Ile	Gln	Trp	Leu	Arg	Lys	Met	Ser	Ser	
174			180					185					190				
176	Asp	Gly	Leu	Gly	Ser	Arg	Ser	Ile	Lys	Gln	Glu	Met	Glu	Glu	Lys	Glu	
177		195					200				205						
179	Asn	Cys	His	Leu	Glu	Gln	Arg	Gln	Val	Lys	Val	Glu	Glu	Pro	Ser	Arg	
180		210				215					220						
182	Pro	Ser	Ala	Ser	Trp	Gln	Asn	Ser	Val	Ser	Glu	Arg	Pro	Pro	Tyr	Ser	
183	225				230					235					240		
185	Tyr	Met	Ala	Met	Ile	Gln	Phe	Ala	Ile	Asn	Ser	Thr	Glu	Arg	Lys	Arg	
186				245					250				255				
188	Met	Thr	Leu	Lys	Asp	Ile	Tyr	Thr	Trp	Ile	Glu	Asp	His	Phe	Pro	Tyr	
189			260				265				270						
191	Phe	Lys	His	Ile	Ala	Lys	Pro	Gly	Trp	Lys	Asn	Ser	Ile	Arg	His	Asn	
192		275					280				285						
194	Leu	Ser	Leu	His	Asp	Met	Phe	Val	Arg	Glu	Thr	Ser	Ala	Asn	Gly	Lys	
195		290				295					300						
197	Val	Ser	Phe	Trp	Thr	Ile	His	Pro	Ser	Ala	Asn	Arg	Tyr	Leu	Thr	Leu	
198	305				310					315					320		
200	Asp	Gln	Val	Phe	Lys	Gln	Gln	Lys	Arg	Pro	Asn	Pro	Glu	Leu	Arg	Arg	
201				325					330				335				
203	Asn	Met	Thr	Ile	Lys	Thr	Glu	Leu	Pro	Leu	Gly	Ala	Arg	Arg	Lys	Met	
204			340						345				350				
206	Lys	Pro	Leu	Leu	Pro	Arg	Val	Ser	Ser	Tyr	Leu	Val	Pro	Ile	Gln	Phe	
207		355				360				365							
209	Pro	Val	Asn	Gln	Ser	Leu	Val	Leu	Gln	Pro	Ser	Val	Lys	Val	Pro	Leu	
210		370				375				380							
212	Pro	Leu	Ala	Ala	Ser	Leu	Met	Ser	Ser	Glu	Leu	Ala	Arg	His	Ser	Lys	
213	385				390					395					400		
215	Arg	Val	Arg	Ile	Ala	Pro	Lys	Val	Leu	Leu	Ala	Glu	Glu	Gly	Ile	Ala	
216			405						410					415			
218	Pro	Leu	Ser	Ser	Ala	Gly	Pro	Gly	Lys	Glu	Glu	Lys	Leu	Leu	Phe	Gly	
219			420					425					430				
221	Glu	Gly	Phe	Ser	Pro	Leu	Leu	Pro	Val	Gln	Thr	Ile	Lys	Glu	Glu	Glu	
222		435					440					445					
224	Ile	Gln	Pro	Gly	Glu	Glu	Met	Pro	His	Leu	Ala	Arg	Pro	Ile	Lys	Val	
225		450				455				460							
227	Glu	Ser	Pro	Pro	Leu	Glu	Glu	Trp	Pro	Ser	Pro	Ala	Pro	Ser	Phe	Lys	
228	465				470					475					480		
230	Glu	Glu	Ser	Ser	His	Ser	Trp	Glu	Asp	Ser	Ser	Gln	Ser	Pro	Thr	Pro	
231				485					490					495			
233	Arg	Pro	Lys	Lys	Ser	Tyr	Ser	Gly	Leu	Arg	Ser	Pro	Thr	Arg	Cys	Val	
234			500					505					510				

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236 Ser Glu Met Leu Val Ile Gln His Arg Glu Arg Arg Glu Arg Ser Arg
237          515          520          525
239 Ser Arg Arg Lys Gln His Leu Leu Pro Pro Cys Val Asp Glu Pro Glu
240          530          535          540
242 Leu Leu Phe Ser Glu Gly Pro Ser Thr Ser Arg Trp Ala Ala Glu Leu
243 545          550          555          560
245 Pro Phe Pro Ala Asp Ser Ser Asp Pro Ala Ser Gln Leu Ser Tyr Ser
246          565          570          575
248 Gln Glu Val Gly Gly Pro Phe Lys Thr Pro Ile Lys Glu Thr Leu Pro
249          580          585          590
251 Ile Ser Ser Thr Pro Ser Lys Ser Val Leu Pro Arg Thr Pro Glu Ser
252          595          600          605
254 Trp Arg Leu Thr Pro Pro Ala Lys Val Gly Gly Leu Asp Phe Ser Pro
255          610          615          620
257 Val Gln Thr Ser Gln Gly Ala Ser Asp Pro Leu Pro Asp Pro Leu Gly
258 625          630          635          640
260 Leu Met Asp Leu Ser Thr Thr Pro Leu Gln Ser Ala Pro Pro Leu Glu
261          645          650          655
263 Ser Pro Gln Arg Leu Leu Ser Ser Glu Pro Leu Asp Leu Ile Ser Val
264          660          665          670
266 Pro Phe Gly Asn Ser Ser Pro Ser Asp Ile Asp Val Pro Lys Pro Gly
267          675          680          685
269 Ser Pro Glu Pro Gln Val Ser Gly Leu Ala Ala Asn Arg Ser Leu Thr
270          690          695          700
272 Glu Gly Leu Val Leu Asp Thr Met Asn Asp Ser Leu Ser Lys Ile Leu
273 705          710          715          720
275 Leu Asp Ile Ser Phe Pro Gly Leu Asp Glu Asp Pro Leu Gly Pro Asp
276          725          730          735
278 Asn Ile Asn Trp Ser Gln Phe Ile Pro Glu Leu Gln
279          740          745

```

281 <210> SEQ ID NO: 3

282 <211> LENGTH: 6

283 <212> TYPE: PRT

284 <213> ORGANISM: Artificial

286 <220> FEATURE:

287 <223> OTHER INFORMATION: FoxM1B LXLXXL motif

289 <220> FEATURE:

290 <221> NAME/KEY: UNSURE

291 <222> LOCATION: (2)..(2)

292 <223> OTHER INFORMATION: X is any amino acid

295 <220> FEATURE:

296 <221> NAME/KEY: UNSURE

297 <222> LOCATION: (4)..(5)

298 <223> OTHER INFORMATION: X is any amino acid

301 <400> SEQUENCE: 3

W--> 303 Leu Xaa Leu Xaa Xaa Leu

304 1 5

306 <210> SEQ ID NO: 4

307 <211> LENGTH: 66

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308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial
311 <220> FEATURE:
312 <223> OTHER INFORMATION: EcoR1 T-epitope tagged FoxM1B primer
314 <400> SEQUENCE: 4
315 gcggaattca ccatggctag catgactggg ggacagcaaa tggggtggca gaactctgtg      60
317 tctgag                                                                66
320 <210> SEQ ID NO: 5
321 <211> LENGTH: 18
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial
325 <220> FEATURE:
326 <223> OTHER INFORMATION: antisense primer for CMV expression vector SV-40 poly A
region
328 <400> SEQUENCE: 5
329 gtttgtccaa ttatgtca                                                    18
332 <210> SEQ ID NO: 6
333 <211> LENGTH: 12
334 <212> TYPE: DNA
335 <213> ORGANISM: Artificial
337 <220> FEATURE:
338 <223> OTHER INFORMATION: FoxM1B/FoxA binding site
340 <400> SEQUENCE: 6
341 tttgtttggt tg                                                            12
344 <210> SEQ ID NO: 7
345 <211> LENGTH: 6
346 <212> TYPE: RNA
347 <213> ORGANISM: Artificial
349 <220> FEATURE:
350 <223> OTHER INFORMATION: transcription termination signal
352 <400> SEQUENCE: 7
353 aauaaa                                                                    6
356 <210> SEQ ID NO: 8
357 <211> LENGTH: 81
358 <212> TYPE: PRT
359 <213> ORGANISM: Homo sapiens
361 <400> SEQUENCE: 8
363 Pro Phe Lys Thr Pro Ile Lys Glu Thr Leu Pro Ile Ser Ser Thr Pro
364 1          5          10          15
366 Ser Lys Ser Val Leu Pro Arg Thr Pro Glu Ser Trp Arg Leu Thr Pro
367          20          25          30
369 Pro Ala Lys Val Gly Gly Leu Asp Phe Ser Pro Val Gln Thr Ser Gln
370          35          40          45
372 Gly Ala Ser Asp Pro Leu Pro Asp Pro Leu Gly Leu Met Asp Leu Ser
373          50          55          60
375 Thr Thr Pro Leu Gln Ser Ala Pro Pro Leu Glu Ser Pro Gln Arg Leu
376 65          70          75          80
378 Leu
381 <210> SEQ ID NO: 9
382 <211> LENGTH: 28

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 2,4,5

Seq#:9; Xaa Pos. 2,3,4,6,8,9,11,12,13,14,16,17,18,19,20,22,23,24,25,26

Seq#:10; Xaa Pos. 1,2,3,4,5,6,7,8,9

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,9

VERIFICATION SUMMARY

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L:303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
M:341 Repeated in SeqNo=9
L:446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0